OM protein - protein search, using sw model

GenCore version 4.5

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Run on: March 1, 2001, 15:52:17 ; Search time 170.72 Seconds
(without alignments)
17.102 Million cell updates/sec

Title: US-09-331-631A-1_COPY_74_116
Perfect score: 248
Sequence: 1 NQEDPQTECOQCQRRCRQQE............RQQQYCQRRCKEICEEEEY 43
Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : PIR_66:*
      1: pir1:*
      2: pir2:*
      3: pir3:*
      4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	117	47.2	566	2	S22477	vicilin precursor
2	105	42.3	588	1	FWCNAB	alpha-globulin B p
3	104	41.9	509	2	S08059	alpha-globulin B p
4	96	38.7	411	2	T29475	hypothetical prote
5	94	37.9	605	2	S06398	alpha-globulin typ
6	80.5	32.5	425	2	T18592	hypothetical prote
7	80.5	32.5	600	2	T18593	alpha-globulin typ
8	80.5	32.5	810	2	T44430	hypothetical prote
9	79	31.9	572	2	T29880	protein PV100 [imp
10	78	31.5	47	2	JC5557	hypothetical prote
11	77.5	31.2	242	2	T29699	arginine/glutamate
12	74	29.8	388	2	T31887	hypothetical prote
13	74	29.8	388	2	T31888	hypothetical prote
14	74	29.8	388	2	T31889	hypothetical prote
15	74	29.8	445	2	T31898	hypothetical prote
16	73.5	29.6	335	2	T31560	hypothetical prote
17	73.5	29.6	335	2	T31561	hypothetical prote
18	72.5	29.2	330	2	T20930	hypothetical prote
19	71.5	28.8	335	2	T25169	hypothetical prote
20	70	28.2	335	2	T31559	hypothetical prote
21	68.5	27.6	1513	2	T23681	hypothetical prote
22	68	27.4	654	2	T30136	hypothetical prote
23	67	27.0	419	2	T18450	hypothetical prote
24	66.5	26.8	154	2	T27967	hypothetical prote
25	66.5	26.8	273	2	T20910	hypothetical prote
26	66.5	26.8	314	2	T27686	hypothetical prote
27	66.5	26.8	637	2	S31574	globulin Beg1 prec
28	65	26.2	111	2	S35221	hypothetical prote
29	65	26.2	910	2	A34721	androgen receptor
30	65	26.2	911	2	B34721	androgen receptor
31	65	26.2	919	2	A39248	androgen receptor
32	65	26.2	1306	2	T13592	hypothetical prote
33	63.5	25.6	33	2	A41822	antimicrobial pept
34	63.5	25.6	51	2	HSMSS1	antimicrobial pept
35	63.5	25.6	51	2	S03997	protamine - mouse
36	62.5	25.2	342	2	JC7110	protamine 1 - rat
37	62	25.0	648	2	JQ1150	brain-specific mem
38	61	24.6	1390	2	T14004	protein kinase (EC
39	61	24.6	223	1	KASHS2	protein kinase - sli
40	60	24.2	1969	2	T08875	trfA protein - EC
41	60	24.2	4957	2	T03455	histidine kinase h
42	60	24.2	5262	2	T03454	ALR protein - huma
43	59.5	24.0	294	2	T23682	ALR protein - huma
44	59.5	24.0	1282	2	JE0120	glycoprotein A - m
45	59	23.8	285	1	I46207	involucrin - dog

ALIGNMENTS

RESULT 1
S22477
vicilin precursor - cacao
C;Species: Theobroma cacao (cacao)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C;Accession: S22477; S22478; S18105; S22050
R;McHenry, L.; Fritz, P.J.
Plant Mol. Biol. 18, 1173-1176, 1992
A;Title: Comparison of the structure and nucleotide sequence of vicilin genes of coco
A;Reference number: S22477; MUID:92288309
A;Accession: S22478
A;Molecule type: mRNA
A;Accession: S22477
A;Molecule type: DNA
A;Residues: 1-452 <MC2>
A;Residues: 1-566 <MCH>
A;Cross-references: EMBL:X62625
A;Accession: S22478
A;Molecule type: mRNA
A;Residues: 1-452 <MC2>
A;Accession: S22477
A;Residues: 1-566 <MCH>
A;Cross-references: EMBL:X62626
A;Genetics:
C;Introns: 211/1; 269/3; 296/3; 391/3; 502/1
C;Superfamily: glycinin
C;Keywords: seed; storage protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-566/Product: vicilin #status predicted <MAT>

Qy   Query Match   47.2%;   Score 117;   DB 2;   Length 566;
      Best Local Similarity   50.0%;   Pred. No. 4.2e-05;
      Matches   20;   Conservative 10;   Mismatches   10;   Indels   0;   Gaps   0;

Qy   2 OEDPQTECOQCQRCRQQESGPROQQYCQRRCKEICEEEE 41
       :|: .| ||:| |:::| |:::::|| ||:|:|:|:|| :|:|
Db 78 EEELQRQYCQCQGRCCOEOQGQREQOCOCQRRCWEQYKEQE 117

RESULT 2
FWCNAB
alpha-globulin B precursor (clone C72) - upland cotton
N;Alternate names: seed storage protein; vicilin precursor
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: A30838; S06911
R;Chlan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III, L.
Plant Mol. Biol. 7, 475-489, 1986
A;Title: Developmental biochemistry of cottonseed embryogenesis and germination XVIII
A;Reference number: A30838
A;Accession: A30838
A;Molecule type: mRNA
A;Residues: 1-588 <CHL>
A;Cross-references: GB:M16891; NID:g167374; PIDN:AAA33071.1; PID:g167375
A;Experimental source: var. Coker 201
R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.

Plant Mol. Biol. 9, 533-546, 1987
A;Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX. Se
A;Reference number: S06398
A;Accession: S06911
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-81 <CH2>
C;Comment: This is a seed storage protein.
A;Superfamily: glycinin
C;Keywords: glycoprotein; seed; storage protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-588/Product: alpha-globulin storage proprotein #status predicted
F;417/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
Qy          Query Match      42.3%;   Score 105;   DB 1;   Length 588;
            Best Local Similarity    47.5%;   Pred. No. 0.00074;
  Matches  19;   Conservative  9;   Mismatches  10;   Indels  2;   Gaps  1;

Qy      3  EDPQTECQQCQRRCRQQEQESGPRQQQYCQRRCKEICEEEEEE 42
           |||   :||:| |||||  :|: |: ||:|||  :| :
Db     81  EDPQRRYEECQQECRQQEE--RQRPQCCQRCLKRFEQEQQ 118
```

RESULT   3
S08059
alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)
N;Alternate names: seed storage protein
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
R;Chlan, C. A.; Borroto, K.; Kamalay, J. A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A;Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX. Se
A;Reference number: S06398
A;Accession: S08059
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-509 <CHL>
A;Superfamily: glycinin

```
Qy          Query Match      41.98%;   Score 104;   DB 2;   Length 509;
            Best Local Similarity    48.7%;   Pred. No. 0.00084;
  Matches  19;   Conservative  8;   Mismatches  10;   Indels  2;   Gaps  1;

Qy      4  DPQTECQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEE 42
           |||  :|||:| |||||  ||||  |:|||||:|:|:||:
Db      1  DPQRRYEECQQECRQEE--RQQPQCCQRCLKRFEQEQQ 37
```

RESULT   4
T29475
hypothetical protein T01D1.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T29475
R;Bradshaw, H.; Wohldmann, P.
submitted to the EMBL Data Library, November 1996
A;Description: The sequence of C. elegans cosmid T01D1.
A;Reference number: Z20623
A;Accession: T29475
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-411 <BRA>
A;Cross-references: EMBL:U80455; PIDN:AAB37887.1; GSPDB:GN00020; CESP:T01D1.6
A;Experimental source: strain Bristol N2; clone T01D1
C;Genetics:
A;Gene: CESP:T01D1.6
A;Map position: 5
A;Introns: 25/3; 304/3
C;Superfamily: gliadin

```
Qy          Query Match      38.7%;   Score 96;   DB 2;   Length 411;
            Best Local Similarity    39.5%;   Pred. No. 0.0048;
  Matches  17;   Conservative  11;   Mismatches  11;   Indels  4;   Gaps  2;

Qy      2  QEDPQTECQQ-CQRRCRQQESGPRQQQYCQRRCKEICEEEEEY 43
           ||  ||:|||  ||| :|:||: : |:|||:|||::|| ::|
Db    138  QQPAQOQCOODCQOAACPQQO---QPQQQCOOCCOTTCQSDDQY 177
```

RESULT   5
S06398
alpha-globulin type A precursor - upland cotton
N;Alternate names: seed storage protein
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
R;Chlan, C. A.; Borroto, K.; Kamalay, J. A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A;Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX.
A;Reference number: S06398
A;Accession: S06398
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-605 <CHL>
A;Superfamily: glycinin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-605/Product: alpha-globulin type A #status predicted <MAT>

```
Qy          Query Match      37.9%;   Score 94;   DB 2;   Length 605;
            Best Local Similarity    35.9%;   Pred. No. 0.01;
  Matches  14;   Conservative  12;   Mismatches  13;   Indels  0;   Gaps  0;

Qy      2  QEDPQTECQQCQRRCRQQESGPRQQQYCQRRCKEICEEE 40
           |:|: |:||||:||:||| |  ||| :||:| |:|: :||:
Db    115  QQOPDKQFKECOORCQOWOEQRPERKQQCVEECREQYQED 153
```

RESULT   6
T18592
hypothetical protein AC3.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T18592
R;McMurray, A.
submitted to the EMBL Data Library, April 1996
A;Reference number: Z18995
A;Accession: T18592
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-425 <WIL>
A;Cross-references: EMBL:Z71177; PIDN:CAA94867.1; GSPDB:GN00023; CESP:AC3.3
A;Experimental source: clone AC3
C;Genetics:
A;Gene: CESP:AC3.3
A;Map position: 5
A;Introns: 18/3
A;Superfamily: gliadin

```
Qy          Query Match      32.5%;   Score 80.5;   DB 2;   Length 425;
            Best Local Similarity    27.9%;   Pred. No. 0.19;
  Matches  17;   Conservative  9;   Mismatches  12;   Indels  23;   Gaps  2;

Qy      2  QEDPQTECQQCQRCR--------QQESGP-------ROQQYCQRRCKEICE 38
           |:|||  ||:|||:|          ||:||          |||||||:|
Db    255  QQPSAPQCOQCQNTCQOAAPVCQOOCAPQCOQOSAPACOQOCQOTSCQQOTOQCCQOQOCTPQCQ 314

Qy     39  E 39
           :
Db    315  Q 315
```

RESULT 7
T18593
hypothetical protein AC3.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
A;Accession: T18593
R;McMurray, A.
submitted to the EMBL Data Library, April 1996
A;Reference number: Z18995
A;Status: preliminary; translated from GB/EMBL/DDBJ
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
A;Molecule type: DNA
A;Residues: 1-600 <WIL>
A;Cross-references: EMBL:Z71177; PIDN:CAA94868.1; GSPDB:GN00023; CESP:AC3.4
A;Experimental source: clone AC3
C;Genetics:
A;Gene: CESP:AC3.4
A;Map position: 5
A;Introns: 292/2; 374/3; 572/2

Query Match   32.5%;   Score 80.5;   DB 2;   Length 600;
Best Local Similarity   27.9%;   Pred. No. 0.25;
Matches 17; Conservative   9; Mismatches   12; Indels   23; Gaps   2;

Qy   2 QEDPQTECQOCQORRCR---------------QOESGP------------RQQQYCQRRCKEICE 38
         :|||||| |||||| |||:| ||:
Db 122 QQPSAPQCOOCOONTCQOOAAPVCQOOCAPCOQOOSAPACCOOOTSCOOTOOCQOOCTPOCO 181

RESULT 8
T44430
protein PV100 [imported] - winter squash
C;Species: Cucurbita maxima (winter squash)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
A;Accession: T44430
R;Yamada, K.; Shimada, T.; Kondo, M.; Nishimura, M.; Hara-Nishimura, I.
J. Biol. Chem. 274, 2263-2570, 1999
A;Title: Multiple functional proteins are produced by cleaving Asn-Gln bonds of a single
A;Reference number: 222767; MUID:99107919
A;Accession: T44430
A;Accession: T44433
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-810 <YAM>
A;Cross-references: EMBL:AB019195; NID:g3808061; PIDN:BAA34056.1; PID:g3808062

Query Match   32.4%;   Score 80.5;   DB 2;   Length 810;
Best Local Similarity   37.2%;   Pred. No. 0.31;
Matches 16; Conservative   9; Mismatches   17; Indels   1; Gaps   1;

Qy   1 NQE-DPQTECQOCQROOESGPROQQYCQRRCKEICEEEEE 42
Db   69 NQRGSPRAEYEVCRLRCQVAERGVEQQORRCEQVCEERLREREQ 111

RESULT 9
T29880
hypothetical protein F19G12.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
A;Accession: T29880
R;Nhan, M.; Le, T.T.
submitted to the EMBL Data Library, April 1996
A;Reference number: Z20704
A;Description: The sequence of C. elegans cosmid F19G12.
A;Accession: T29880
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-572 <NHA>
A;Cross-references: EMBL:U51997; PIDN:AAC48159.1; GSPDB:GN00028; CESP:F19G12.7
A;Experimental source: strain Bristol N2; clone F19G12
C;Genetics:
A;Gene: CESP:F19G12.7
A;Map position: X
A;Introns: 18/3

Query Match   31.9%;   Score 79;   DB 2;   Length 572;
Best Local Similarity   34.0%;   Pred. No. 0.34;
Matches 17; Conservative   8; Mismatches   7; Indels   18; Gaps   3;

Qy   8 ECQOCQORRCRQ--------------QOESGPRQQQYCQRRCKE---ICEEE 40
         |||||| |:| || || |:| :||::
Db 381 OCQOCQONTCQOFAPVCEQOCASLCHOPSAPOCQO-CONTCQOFAPVCEQO 429

RESULT 10
JC5557
arginine/glutamate-rich 6.5k polypeptide - smooth loofah
C;Species: Luffa cylindrica (smooth loofah)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 07-May-1999
A;Accession: JC5557
R;Kimura, M.; Park, S.S.; Sakai, R.; Yamasaki, N.; Funatsu, G.
Biosci. Biotechnol. Biochem. 61, 984-988, 1997
A;Title: Primary structure of 6.5k-arginine/glutamate-rich polypeptide from the seeds
A;Reference number: JC5557; MUID:97357433
A;Accession: JC5557
A;Molecule type: protein
A;Residues: 1-47 <KIM>
A;Experimental source: seed
A;Comment: This protein is a storage protein which provides nitrogen and carbon reser
F;12-33,16-29/Disulfide bonds: #status predicted

Query Match   31.5%;   Score 78;   DB 2;   Length 47;
Best Local Similarity   40.0%;   Pred. No. 0.07;
Matches 14; Conservative   9; Mismatches   8; Indels   4; Gaps   1;

Qy   5 PQTECQOCQORRCRQOESGPRQQQYCQRRCKEICEE 39
         ||| ||| ||:::||:   :||:||
Db   5 PRTEYEACRVRCQVAEHGVER----QRRCQVCEK 35

RESULT 11
T29699
hypothetical protein F31A3.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
A;Accession: T29699
R;Murray, J.; Le, T.T.
submitted to the EMBL Data Library, May 1996
A;Reference number: Z20667
A;Description: The sequence of C. elegans cosmid F31A3.
A;Accession: T29699
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-242 <MUR>
A;Cross-references: EMBL:U58742; PIDN:AAB36856.1; GSPDB:GN00028; CESP:F31A3.1
A;Experimental source: strain Bristol N2; clone F31A3
C;Genetics:
A;Gene: CESP:F31A3.1
A;Map position: X
A;Introns: 18/3; 160/3
C;Superfamily: ultra-high-sulfur keratin

Query Match   31.2%;   Score 77.5;   DB 2;   Length 242;
Best Local Similarity   33.3%;   Pred. No. 0.26;
Matches 17; Conservative   12; Mismatches   11; Indels   11; Gaps   4;

RESULT 12
```
Qy   2 QEDPQTECQQCQQRRCR------QQESGPR-QQQY---CQRRCKEICEEEEE 42
         : |||||  |||:||          ::   |: :|  ||:::|  :: ::
Db  77 QQPAAPQCQQCONTCQQSAPVCQQQCAPCQQQQFAPACQ-QCQNSCQQTQQ 126
```

T31887
hypothetical protein C03A7.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
A;Accession: T31887
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
R;Greco, T.; Bradshaw, H.; Elliott, G.
A;Accession: T31887
A;Description: The sequence of C. elegans cosmid C03A7.
submitted to the EMBL Data Library, July 1997
A;Reference number: Z21096
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-388 <GRE>
A;Cross-references: EMBL:AF016451; PIDN:AAB66001.1; GSPDB:GN00023; CESP:C03A7.4
A;Experimental source: strain Bristol N2; clone C03A7
C;Genetics:
A;Gene: CESP:C03A7.4
A;Map position: 5
A;Introns: 75/3
C;Superfamily: gliadin

```
Query Match     29.8%;  Score 74;  DB 2;  Length 388;
Best Local Similarity   30.2%;  Pred. No. 0.84;
Matches    13;  Conservative    12;  Mismatches    12;  Indels    6;  Gaps    2;

Qy   3 EDPQTECQ-QCQQRRC-----RQQESGPRQQQYCQRRCKEICEE 39
         |:||  ||| ||||:|           ::|||  |:|::::
Db 191 QQAQAQCQPQCQQCQSSCVQQQQQSNQCEPACNTQCSDICQQ 233
```

RESULT 13
T31888
hypothetical protein C03A7.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
R;Greco, T.; Bradshaw, H.; Elliott, C.
A;Accession: T31888
A;Description: The sequence of C. elegans cosmid C03A7.
submitted to the EMBL Data Library, July 1997
A;Reference number: Z21096
A;Accession: T31888
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-388 <GRE>
A;Cross-references: EMBL:AF016451; PIDN:AAB65996.1; GSPDB:GN00023; CESP:C03A7.7
A;Experimental source: strain Bristol N2; clone C03A7
C;Genetics:
A;Gene: CESP:C03A7.7
A;Map position: 5
A;Introns: 75/3
C;Superfamily: gliadin

```
Query Match     29.8%;  Score 74;  DB 2;  Length 388;
Best Local Similarity   30.2%;  Pred. No. 0.84;
Matches    13;  Conservative    12;  Mismatches    12;  Indels    6;  Gaps    2;

Qy   3 EDPQTECQ-QCQRRC-----RQQESGPRQQQYCQRRCKEICEE 39
         :|| :||||:||:|           ::|||  |:|::::
Db 191 QQAQAQCQPQCQQCQSSCVQQQQQSNQCEPACNTQCSDICQQ 233
```

RESULT 14
T31889
hypothetical protein C03A7.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans

RESULT 15
T31898
hypothetical protein C03A7.14 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
R;Greco, T.; Bradshaw, H.; Elliott, G.
C;Accession: T31898
submitted to the EMBL Data Library, July 1997
A;Reference number: Z21096
A;Accession: T31898
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-445 <GRE>
A;Cross-references: EMBL:AF016451; PIDN:AAB65007.1; GSPDB:GN00023; CESP:C03A7.14
A;Experimental source: strain Bristol N2; clone C03A7
C;Genetics:
A;Gene: CESP:C03A7.14
A;Map position: 5
A;Introns: 18/3; 75/3
C;Superfamily: gliadin

```
Query Match     29.8%;  Score 74;  DB 2;  Length 438;
Best Local Similarity   30.2%;  Pred. No. 0.92;
Matches    13;  Conservative    12;  Mismatches    12;  Indels    6;  Gaps    2;

Qy   3 EDPQTECQ-QCQRRC-----RQQESGPRQQQYCQRRCKEICEE 39
         :|| :||||:||:|           ::|||  |:|::::
Db 191 QQAQAQCQPQCQQCQSSCVQQQQOPSTQCEPACNTQCSDICQQ 233
```

Search completed: March 1, 2001, 15:52:19
Job time: 543 sec